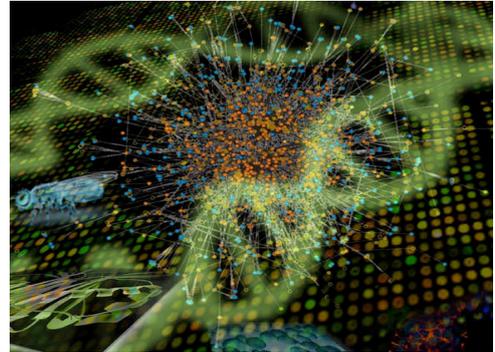


# Post-Doctoral position – Bioinformatics

## Logic and dynamics of transcription and epigenetics during cell fate decisions

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Transcriptional networks are a key driving force in development, evolution and disease, yet how they generate robust yet dynamic outcomes remains elusive. The Furlong group's research focuses on dissecting general mechanisms by which transcription and regulatory networks function during embryonic development. For this purpose, her work combines genomic, genetic and computational approaches to understand (1) the general principles of how *cis*-regulatory elements control complex patterns of temporal and spatial activity; (2) to gain an understanding of how robust developmental progression is achieved; and (3) to build predictive models of gene expression

The Furlong lab is composed of both wet lab biologists and computational biologists, generating a creative environment to promote collaborations and test computational predictions. EMBL is a highly international multidisciplinary institute where the working language is English.

### **Recent publications:**

1. Rembold M, et al (2014). **Genes & Dev.** Jan 15;28(2):167. Top 5 most downloaded article in January
2. Erceg J, et al (2014). **PLoS Genet.** Jan;10(1):e1004060.
3. Spitz F and Furlong EE (2012). **Nature Reviews Genetics**, Sep;13(9):613-26.
4. Junion G\*, Spivakov M\*, et al (2012). **Cell**, Feb 3;148(3):473-86.
5. Bonn S\*, Zinzen RP\*, Girardot C\*, et al (2012). **Nature Genetics**, Jan 8;44(2):148-56
6. Zinzen RP\*, Girardot C\*, Gagneur J\*, et al. (2009). **Nature**. 2009 Nov 5;462(7269):65-70.

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